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☐ 1: P54926 **MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (IMPASE 1) (IMP 1) (INOSITOL MONOPHOSPHATASE 1)** BLink, PubMed, Related Sequences, Taxonomy

LOCUS MYO1\_LYCES 273 aa PLN 01-OCT-2000  
 DEFINITION MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (IMPASE 1) (IMP 1) (INOSITOL MONOPHOSPHATASE 1).  
 ACCESSION P54926  
 PID g1709203  
 VERSION P54926 GI:1709203  
 DBSOURCE swissprot: locus MYO1\_LYCES, accession P54926;  
 class: standard.  
 created: Oct 1, 1996.  
 sequence updated: Oct 1, 1996.  
 annotation updated: Oct 1, 2000.  
 xrefs: gi: 1098976, gi: 1098977  
 xrefs (non-sequence databases): HSSP P29218, InterPro IPR000760,  
 Pfam PF00459, PRINTS PR00378, PROSITE PS00629, PROSITE PS00630  
 KEYWORDS Hydrolase; Magnesium; Lithium; Multigene family.  
 SOURCE tomato.  
 ORGANISM *Lycopersicon esculentum*  
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids  
 I; Solanales; Solanaceae; Solanum; Lycopersicon.  
 REFERENCE 1 (residues 1 to 273)  
 AUTHORS Gillasp, G.E., Keddle, J.S., Oda, K. and Gruissem, W.  
 TITLE Plant inositol monophosphatase is a lithium-sensitive enzyme  
 encoded by a multigene family  
 JOURNAL Plant Cell 7 (12), 2175-2185 (1995)  
 MEDLINE 96351935  
 REMARK SEQUENCE FROM N.A.  
 STRAIN=CV. VFNT CHERRY

## COMMENT

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 the EMBL outstation - the European Bioinformatics Institute.  
 The original entry is available from <http://www.expasy.ch/sprot>  
 and <http://www.ebi.ac.uk/sprot>  
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[FUNCTION] IT IS RESPONSIBLE FOR THE PROVISION OF INOSITOL REQUIRED  
 FOR SYNTHESIS OF PHOSPHATIDYLINOSITOL AND POLYPHOSPHOINOSITIDES.  
 [CATALYTIC ACTIVITY] MYO-INOSITOL 1-MONOPHOSPHATE + H(2)O =  
 MYO-INOSITOL + ORTHOPHOSPHATE.  
 [COFACTOR] REQUIRES MAGNESIUM (BY SIMILARITY).  
 [ENZYME REGULATION] INHIBITED BY LI(+).  
 [PATHWAY] KEY ENZYME OF THE PHOSPHATIDYL INOSITOL SIGNALING  
 PATHWAY.  
 [SIMILARITY] BELONGS TO THE INOSITOL MONOPHOSPHATASE FAMILY.

## FEATURES

source

Location/Qualifiers

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/organism="Lycopersicon esculentum"

Protein      /db\_xref="taxon:4081"  
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             /EC\_number="3.1.3.25"

## ORIGIN

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Search		Protein	for				
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☐ 1: **P74158 EXTRAGENIC SUPPRESSOR** BLink, PubMed, Related Sequences, Taxonomy  
**PROTEIN SUHB HOMOLOG**

LOCUS SUHB\_SYNY3 287 aa ·BCT 15-DEC-1998  
 DEFINITION EXTRAGENIC SUPPRESSOR PROTEIN SUHB HOMOLOG.   
 ACCESSION P74158  
 PID g3915048  
 VERSION P74158 GI:3915048  
 DBSOURCE swissprot: locus SUHB\_SYNY3, accession P74158;  
 class: standard.  
 created: Dec 15, 1998.  
 sequence updated: Dec 15, 1998.  
 annotation updated: Dec 15, 1998.  
 xrefs: gi: gi: 1653228, gi: gi: 1653332  
 xrefs (non-sequence databases): PFAM PF00459, PROSITE PS00629,  
 PROSITE PS00630

KEYWORDS .  
 SOURCE Synechocystis PCC6803.  
 ORGANISM Synechocystis PCC6803  
 Bacteria; Cyanobacteria; Chroococcales; Synechocystis.

REFERENCE 1 (residues 1 to 287)  
 AUTHORS KANEKO,T., SATO,S., KOTANI,H., TANAKA,A., ASAMIZU,E., NAKAMURA,Y.,  
 MIYAJIMA,N., HIROSAWA,M., SUGIURA,M., SASAMOTO,S., KIMURA,T.,  
 HOSOUCHI,T., MATSUNO,A., MURAKI,A., NAKAZAKI,N., NARUO,K.,  
 OKUMURA,S., SHIMPO,S., TAKEUCHI,C., WADA,T., WATANABE,A.,  
 YAMADA,M., YASUDA,M. and TABATA,S.  
 TITLE Sequence analysis of the genome of the unicellular cyanobacterium  
 Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 entire genome and assignment of potential protein-coding regions  
 JOURNAL DNA Res. 3 (3), 109-136 (1996)  
 MEDLINE 97061201  
 REMARK SEQUENCE FROM N.A.  
 COMMENT

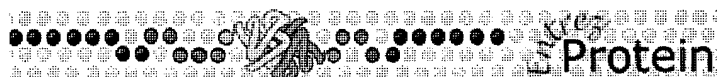
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 collaboration between the Swiss Institute of Bioinformatics and  
 the EMBL outstation - the European Bioinformatics Institute.  
 The original entry is available from <http://www.expasy.ch/sprot>  
 and <http://www.ebi.ac.uk/sprot>  
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[SIMILARITY] BELONGS TO THE INOSITOL MONOPHOSPHATASE FAMILY.

FEATURES Location/Qualifiers  
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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search	Protein	for					Go Clear
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☐ 1: **BAA17860 extragenic suppressor [Synechocystis sp.]** BLink, PubMed, Related Sequences, Nucleotide, Genome, Ta

LOCUS BAA17860 267 aa BCT 07-FEB-1999  
 DEFINITION extragenic suppressor [Synechocystis sp.].  
 ACCESSION BAA17860  
 PID g1652942  
 VERSION BAA17860.1 GI:1652942  
 DBSOURCE locus D90909 accession D90909.1  
 KEYWORDS .  
 SOURCE Synechocystis sp.  
 ORGANISM Synechocystis sp.  
 Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 REFERENCE 1 (sites)  
 AUTHORS Kaneko,T., Sato,S., Kotani,H., Tanaka,A., Asamizu,E., Nakamura,Y., Miyajima,N., Hirose,M., Sugiura,M., Sasamoto,S., Kimura,T., Hosouchi,T., Matsuno,A., Muraki,A., Nakazaki,N., Naruo,K., Okumura,S., Shimpo,S., Takeuchi,C., Wada,T., Watanabe,A., Yamada,M., Yasuda,M. and Tabata,S.  
 TITLE Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions  
 JOURNAL DNA Res. 3 (3), 109-136 (1996)  
 MEDLINE 97061201  
 REFERENCE 2 (residues 1 to 267)  
 AUTHORS Tabata,S.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-JUN-1996) Satoshi Tabata, Kazusa DNA Research Institute, Laboratory of Gene Structure 2; 1523-3, Yanauchino, Kisarazu, Chiba 292, Japan (E-mail:tabata@kazusa.or.jp, Tel:+81-438-52-3933, Fax:+81-438-52-3934)  
 COMMENT Potential protein coding regions were assigned on the basis of similarity search of the ORFs and GeneMark analysis.  
 FEATURES Location/Qualifiers  
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 181 iyrqqrtaf ggdcfnylsa asgwatmplv iveadlnfyd fcalipiltg anycftdwqg  
 241 keltpestev vaspnklhs eilaflq

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Search		Protein	for				Go Clear
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Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: **P54928 MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 3 (IMPASE 3) (IMP 3) (INOSITOL MONOPHOSPHATASE 3)** BLink, PubMed, Related Sequences, Taxonomy

LOCUS MYO3\_LYCES 268 aa PLN 01-OCT-2000  
 DEFINITION MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 3 (IMPASE 3) (IMP 3) (INOSITOL MONOPHOSPHATASE 3).  
 ACCESSION P54928  
 PID g1709205  
 VERSION P54928 GI:1709205  
 DBSOURCE swissprot: locus MYO3\_LYCES, accession P54928;  
 class: standard.  
 created: Oct 1, 1996.  
 sequence updated: Oct 1, 1996.  
 annotation updated: Oct 1, 2000.  
 xrefs: gi: 1098970, gi: 1098971  
 xrefs (non-sequence databases): HSSP P29218, InterPro IPR000760, Pfam PF00459, PRINTS PR00378, PROSITE PS00629, PROSITE PS00630  
 KEYWORDS Hydrolase; Magnesium; Lithium; Multigene family.  
 SOURCE tomato.  
 ORGANISM *Lycopersicon esculentum*  
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.  
 REFERENCE 1 (residues 1 to 268)  
 AUTHORS Gillasp, G.E., Keddie, J.S., Oda, K. and Gruissem, W.  
 TITLE Plant inositol monophosphatase is a lithium-sensitive enzyme encoded by a multigene family  
 JOURNAL Plant Cell 7 (12), 2175-2185 (1995)  
 MEDLINE 96351935  
 REMARK SEQUENCE FROM N.A.  
 STRAIN=CV. VFNT CHERRY

COMMENT -----  
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[FUNCTION] IT IS RESPONSIBLE FOR THE PROVISION OF INOSITOL REQUIRED FOR SYNTHESIS OF PHOSPHATIDYLINOSITOL AND POLYPHOSPHOINOSITIDES.  
 [CATALYTIC ACTIVITY] MYO-INOSITOL 1-MONOPHOSPHATE + H(2)O = MYO-INOSITOL + ORTHOPHOSPHATE.  
 [COFACTOR] REQUIRES MAGNESIUM (BY SIMILARITY).  
 [ENZYME REGULATION] INHIBITED BY LI(+).  
 [PATHWAY] KEY ENZYME OF THE PHOSPHATIDYL INOSITOL SIGNALING PATHWAY.  
 [SIMILARITY] BELONGS TO THE INOSITOL MONOPHOSPHATASE FAMILY.

FEATURES  
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Protein      /db\_xref="taxon:4081"  
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             /EC\_number="3.1.3.25"

## ORIGIN

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